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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: FLECKENSTEIN, Bernhard  
ALBRECHT, Jens-Christian  
NEIPEL, Frank  
———FRIEDMAN-KIEN, Alvin  
HUANG, Yao-Qi
- (ii) TITLE OF INVENTION: VIRAL INTERLEUKIN-6
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: FOLEY & LARDNER
  - (B) STREET: 3000 K Street, N.W.
  - (C) CITY: Washington
  - (D) STATE: D.C.
  - (E) COUNTRY: U.S.A.
  - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: US 09/230,048
  - (B) FILING DATE: 12-MAR-1999
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: WO PCT/EP96/03199
  - (B) FILING DATE: 19-JUL-1996
- (viii) ATTORNEY/AGENT INFORMATION:
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  - (C) REFERENCE/DOCKET NUMBER: 058315/0129
- (ix) TELECOMMUNICATION INFORMATION:
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  - (B) TELEFAX: (202) 672-5399

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 612 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 1..612

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TGC TGG TTC AAG TTG TGG TCT CTC TTG CTG GTC GGT TCA CTG CTG	48
Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Leu Val Gly Ser Leu Leu	
1 5 10 15	
GTA TCT GGA ACG CGG GGC AAG TTG CCG GAC GCC CCC GAG TTT GAA AAG	96
Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys	
20 25 30	
GAT CTT CTC ATT CAG AGA CTC AAT TGG ATG CTA TGG GTG ATC GAT GAA	144
Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu	
35 40 45	
TGC TTC CGC GAC CTC TGT TAC CGT ACC GGC ATC TGC AAG GGT ATT CTA	192
Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu	
50 55 60	
GAG CCC GCT GCT ATT TTT CAT CTG AAA CTA CCA GCC ATC AAC GAT ACT	240
Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr	
65 70 75 80	
GAT CAC TGC GGG TTA ATA GGA TTT AAT GAG ACT AGC TGC CTT AAA AAG	288
Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys	
85 90 95	
CTC GCC GAT GGC TTT TTT GAA TTC GAG GTG TTG TTT AAG TTT TTA ACG	336
Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr	
100 105 110	
ACG GAG TTT GGA AAA TCA GTG ATA AAC GTG GAC GTC ATG GAG CTT CTG	384
Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu	
115 120 125	
ACG AAG ACC TTA GGA TGG GAC ATA CAG GAA GAG CTC AAT AAG CTG ACT	432
Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr	
130 135 140	
AAG ACG CAC TAC AGT CCA CCC AAA TTT GAC CGC GGT CTA TTA GGG AGG	480
Lys Thr His Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg	
145 150 155 160	
CTT CAG GGA CTT AAG TAT TGG GTG AGA CAC TTT GCT TCG TTT TAT GTT	528
Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val	
165 170 175	
CTG AGT GCA ATG GAA AAG TTT GCA GGT CAA GCG GTG CGT GTT TTG GAC	576
Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp	
180 185 190	
TCT ATC CCA GAC GTG ACT CCT GAC GTC CAC GAT AAG	612
Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys	
195 200	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Cys Trp Phe Lys Leu Trp Ser Leu Leu Leu Val Gly Ser Leu Leu  
1 5 10 15  
Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe Glu Lys  
20 25 30  
Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val Ile Asp Glu  
35 40 45  
Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys Lys Gly Ile Leu  
50 55 60  
Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro Ala Ile Asn Asp Thr  
65 70 75 80  
Asp His Cys Gly Leu Ile Gly Phe Asn Glu Thr Ser Cys Leu Lys Lys  
85 90 95  
Leu Ala Asp Gly Phe Phe Glu Phe Glu Val Leu Phe Lys Phe Leu Thr  
100 105 110  
Thr Glu Phe Gly Lys Ser Val Ile Asn Val Asp Val Met Glu Leu Leu  
115 120 125  
Thr Lys Thr Leu Gly Trp Asp Ile Gln Glu Glu Leu Asn Lys Leu Thr  
130 135 140  
Lys Thr His Tyr Ser Pro Pro Lys Phe Asp Arg Gly Leu Leu Gly Arg  
145 150 155 160  
Leu Gln Gly Leu Lys Tyr Trp Val Arg His Phe Ala Ser Phe Tyr Val  
165 170 175  
Leu Ser Ala Met Glu Lys Phe Ala Gly Gln Ala Val Arg Val Leu Asp  
180 185 190  
Ser Ile Pro Asp Val Thr Pro Asp Val His Asp Lys  
195 200

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 212 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu  
1 5 10 15  
Gly Leu Leu Leu Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro  
20 25 30  
Gly Glu Asp Ser Lys Asp Val Ala Ala Pro His Arg Gln Pro Leu Thr  
35 40 45

Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile Leu Asp Gly Ile  
 50 55 60  
 Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser  
 65 70 75 80  
 Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala  
 85 90 95  
 Glu Lys Asp Gly Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Cys Leu  
 100 105 110  
 Val Lys Ile Ile Thr Gly Leu Leu Glu Phe Glu Val Tyr Leu Glu Tyr  
 115 120 125  
 Leu Gln Asn Arg Phe Glu Ser Ser Glu Glu Gln Ala Arg Ala Val Gln  
 130 135 140  
 Met Ser Thr Lys Val Leu Ile Gln Phe Leu Gln Lys Lys Ala Lys Asn  
 145 150 155 160  
 Leu Asp Ala Ile Thr Thr Pro Asp Pro Thr Thr Asn Ala Ser Leu Leu  
 165 170 175  
 Thr Lys Leu Gln Ala Gln Asn Gln Trp Leu Gln Asp Met Thr Thr His  
 180 185 190  
 Leu Ile Leu Arg Ser Phe Lys Glu Phe Leu Gln Ser Ser Leu Arg Ala  
 195 200 205  
 Leu Arg Gln Met  
 210

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 211 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Lys Phe Leu Ser Ala Arg Asp Phe His Pro Val Ala Phe Leu Gly  
 1 5 10 15  
 Leu Met Leu Val Thr Thr Thr Ala Phe Pro Thr Ser Gln Val Arg Arg  
 20 25 30  
 Gly Asp Phe Thr Glu Asp Thr Thr Pro Asn Arg Pro Val Tyr Thr Thr  
 35 40 45  
 Ser Gln Val Gly Gly Leu Ile Thr His Val Leu Trp Glu Ile Val Glu  
 50 55 60  
 Met Arg Lys Glu Leu Cys Asn Gly Asn Ser Asp Cys Met Asn Asn Asp  
 65 70 75 80

Asp	Ala	Leu	Ala	Glu	Asn	Asn	Leu	Lys	Leu	Pro	Glu	Ile	Gln	Arg	Asn	
				85					90					95		
Asp	Gly	Cys	Tyr	Gln	Thr	Gly	Tyr	Asn	Gln	Glu	Ile	Cys	Leu	Leu	Lys	
			100					105					110			
Ile	Ser	Ser	Gly	Leu	Leu	Glu	Tyr	His	Ser	Tyr	Leu	Glu	Tyr	Met	Lys	
		115					120					125				
Asn	Asn	Leu	Lys	Asp	Asn	Lys	Lys	Asp	Lys	Ala	Arg	Val	Leu	Gln	Arg	
		130				135					140					
Asp	Thr	Glu	Thr	Leu	Ile	His	Ile	Phe	Asn	Gln	Glu	Val	Lys	Asp	Leu	
145					150					155					160	
His	Lys	Ile	Val	Leu	Pro	Thr	Pro	Ile	Ser	Asn	Ala	Leu	Leu	Thr	Asp	
			165						170					175		
Lys	Leu	Glu	Ser	Gln	Lys	Glu	Trp	Leu	Arg	Thr	Lys	Thr	Ile	Gln	Phe	
			180					185					190			
Ile	Leu	Lys	Ser	Leu	Glu	Glu	Phe	Leu	Lys	Val	Thr	Leu	Arg	Ser	Thr	
		195					200					205				
Arg	Gln	Thr														
		210														